

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:02:12 ; Search time 113.536  
Seconds

(without alignments)  
5591.830 Million cell

updates/sec

Title: US-09-300-482-298  
Perfect score: 388  
Sequence: 1  
ggagaaagaaagaaaagatg.....ttaaagcctgggacccccgt 388

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to  
have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

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